

# SEQUENCE LISTING

<110> Sode, Koji

<120> GLUCOSE DEHYDROGENASE/CYTOCHROME FUSION PROTEIN

<130> 3691-0130PUS1

<140> US 10/574,085

<141> 2006-03-30

<150> PCT/JP2004/014575

<151> 2004-09-28

<150> JP 2003-340092

<151> 2003-09-30

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 1776

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA coding for a fusion protein

<400> 1

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tttgacaaga	aagttattct	atctaattcta	aataagccgc	atgctttgtt	atggggacca	180
gataatcaaa	tttggttaac	tgagcgagca	acaggttaaga	ttctaagagt	taatccagag	240
tcgggtagtg	taaaaacagt	ttttcaggta	ccagagattg	tcaatgatgc	tgatgggcag	300
aatggtttat	taggttttgc	cttccatcct	gatttttaaaa	ataatcctta	tatctatatt	360
tcagggtacat	ttaaaaatcc	gaaatctaca	gataaagaat	taccgaacca	aacgattatt	420
cgtcgttata	cctataataa	atcaacagat	acgctcgaga	agccagtcga	tttattagca	480
ggattacctt	catcaaaaga	ccatcagtc	ggtcgtcttg	tcattgggcc	agatcaaaag	540
at ttattata	cgattgggtga	ccaagggcgt	aaccagcttg	cttattttgtt	cttgccaaat	600
caagcacaaac	atacgccaac	tcaacaagaa	ctgaatggta	aagactatca	cacctatatg	660
ggtaaagtac	tacgcttaaa	tcttgatgga	agtattccaa	aggataatcc	aagtttttaac	720
gggggtgggt	gccatattta	tacacttgga	catcgtaatc	cgcagggtct	agcattcact	780
ccaaatggta	aattattgca	gtctgaacaa	ggcccaaact	ctgacgatga	aattaacctc	840
attgtcaaag	gtggcaatta	tggttgccg	aatgtagcag	gttataaaga	tgatagtggc	900
tatgcttatg	caaattattc	agcagcagcc	aataagtcaa	ttaaggattt	agctcaaaat	960
ggagtaaaag	tagccgcagg	ggtcctgtg	acgaaagaat	ctgaatggac	tggtaaaaac	1020
tttgtcccac	cattaaaaac	tttatatacc	gttcaagata	cctacaacta	taacgatcca	1080
acttgtggag	agatgaccta	catttgctgg	ccaacagttg	caccgtcatc	tgccctatgtc	1140
tataagggcg	gtaaaaaagc	aattactggg	tgggaaaata	cattattggg	tccatcttta	1200
aaacgtgggtg	tcatttttccg	tattaagtta	gatccaactt	atagcactac	ttatgatgac	1260
gctgtaccga	tggttaagag	caacaaccgt	tatcgtgatg	tgattgcaag	tccagatggg	1320
aatgtcttat	atgtattaac	tgatactgcc	ggaaatgtcc	aaaaagatga	tggtcagta	1380
acaaatacat	tagaaaaccc	aggatctctc	attaagttca	cctataaggc	taaggagctc	1440
ggcaaggcca	ggatgccgga	gttcgtggcc	cagcgcaccg	gccagttgct	gcagggcggtg	1500
aaatacgacc	ccgccaaggt	cgaggccggc	accatgctgt	atgtggccaa	ctgcgttttc	1560
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gcgagctata tcgagaacct gccaaacttt gtcttcaagg gcccgcccat ggtgcgcggc 1680
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<210> 2
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<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic fusion protein

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<400> 2
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20 25 30
Phe Ala Lys Ala Lys Ser Glu Asn Phe Asp Lys Lys Val Ile Leu Ser
35 40 45
Asn Leu Asn Lys Pro His Ala Leu Leu Trp Gly Pro Asp Asn Gln Ile
50 55 60
Trp Leu Thr Glu Arg Ala Thr Gly Lys Ile Leu Arg Val Asn Pro Glu
65 70 75 80
Ser Gly Ser Val Lys Thr Val Phe Gln Val Pro Glu Ile Val Asn Asp
85 90 95
Ala Asp Gly Gln Asn Gly Leu Leu Gly Phe Ala Phe His Pro Asp Phe
100 105 110
Lys Asn Asn Pro Tyr Ile Tyr Ile Ser Gly Thr Phe Lys Asn Pro Lys
115 120 125
Ser Thr Asp Lys Glu Leu Pro Asn Gln Thr Ile Ile Arg Arg Tyr Thr
130 135 140
Tyr Asn Lys Ser Thr Asp Thr Leu Glu Lys Pro Val Asp Leu Leu Ala
145 150 155 160
Gly Leu Pro Ser Ser Lys Asp His Gln Ser Gly Arg Leu Val Ile Gly
165 170 175
Pro Asp Gln Lys Ile Tyr Tyr Thr Ile Gly Asp Gln Gly Arg Asn Gln
180 185 190
Leu Ala Tyr Leu Phe Leu Pro Asn Gln Ala Gln His Thr Pro Thr Gln
195 200 205
Gln Glu Leu Asn Gly Lys Asp Tyr His Thr Tyr Met Gly Lys Val Leu
210 215 220
Arg Leu Asn Leu Asp Gly Ser Ile Pro Lys Asp Asn Pro Ser Phe Asn
225 230 235 240
Gly Val Val Ser His Ile Tyr Thr Leu Gly His Arg Asn Pro Gln Gly
245 250 255
Leu Ala Phe Thr Pro Asn Gly Lys Leu Leu Gln Ser Glu Gln Gly Pro
260 265 270
Asn Ser Asp Asp Glu Ile Asn Leu Ile Val Lys Gly Gly Asn Tyr Gly
275 280 285
Trp Pro Asn Val Ala Gly Tyr Lys Asp Asp Ser Gly Tyr Ala Tyr Ala
290 295 300
Asn Tyr Ser Ala Ala Ala Asn Lys Ser Ile Lys Asp Leu Ala Gln Asn
305 310 315 320
Gly Val Lys Val Ala Ala Gly Val Pro Val Thr Lys Glu Ser Glu Trp
325 330 335
Thr Gly Lys Asn Phe Val Pro Pro Leu Lys Thr Leu Tyr Thr Val Gln

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	340		345		350
Asp Thr Tyr Asn Tyr Asn Asp Pro Thr Cys Gly Glu Met Thr Tyr Ile					
	355		360		365
Cys Trp Pro Thr Val Ala Pro Ser Ser Ala Tyr Val Tyr Lys Gly Gly					
	370		375		380
Lys Lys Ala Ile Thr Gly Trp Glu Asn Thr Leu Leu Val Pro Ser Leu					
385		390		395	400
Lys Arg Gly Val Ile Phe Arg Ile Lys Leu Asp Pro Thr Tyr Ser Thr					
	405		410		415
Thr Tyr Asp Asp Ala Val Pro Met Phe Lys Ser Asn Asn Arg Tyr Arg					
	420		425		430
Asp Val Ile Ala Ser Pro Asp Gly Asn Val Leu Tyr Val Leu Thr Asp					
	435		440		445
Thr Ala Gly Asn Val Gln Lys Asp Asp Gly Ser Val Thr Asn Thr Leu					
	450		455		460
Glu Asn Pro Gly Ser Leu Ile Lys Phe Thr Tyr Lys Ala Lys Glu Leu					
465		470		475	480
Gly Lys Ala Arg Met Pro Glu Phe Val Ala Gln Arg Thr Gly Gln Leu					
	485		490		495
Leu Gln Gly Val Lys Tyr Asp Pro Ala Lys Val Glu Ala Gly Thr Met					
	500		505		510
Leu Tyr Val Ala Asn Cys Val Phe Cys His Gly Val Pro Gly Val Asp					
	515		520		525
Arg Gly Gly Asn Ile Pro Asn Leu Gly Tyr Met Asp Ala Ser Tyr Ile					
	530		535		540
Glu Asn Leu Pro Asn Phe Val Phe Lys Gly Pro Ala Met Val Arg Gly					
545		550		555	560
Met Pro Asp Phe Thr Gly Lys Leu Ser Gly Asp Asp Val Glu Ser Leu					
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Lys Ala Phe Ile Gln Gly Thr Ala Asp Ala Ile Arg Pro Lys Pro					
	580		585		590

<210> 3  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 3  
 ggccatggat aaacatttat tggctaaaat tgctttat

38

<210> 4  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 4  
 gggggagctc cttagcctta taggtgaac

29

<210> 5  
 <211> 30  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 5

gggggagctc ggcaaggcca ggatgccgga

30

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 6

ggggaagctt tcagggcttg ggccggatgg

30